Student ID

Your topic: Several incorrect models of DNA structure were explored, by Watson and others, before Watson and crick settled on the correct structure. write an essay explaining three of these incorrect structures, how and why they were developed, and what evidence eventually to each being discarded

Your topic's description:it's about the double helix book by James D.Watson

Your desired style of citation: Harvard Referencing

Your educational level: Guaranteed 2:2 Standard

Referencing Style: Harvard Referencing

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Models of DNA Structure

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[Name of the Supervisor]

[Course]

Seriesof worksranging from1928 to 1952allowinvolvingDNAdefinitivelythe notion ofgenetic information.Despite agrowing body of evidenceto the early50s, the scientific community did not acceptеasilythat DNAcould be thebasis of heredity. According to thethesisthenthe most widely accepted, DNA isasingle molecule, and therefore unable toconveycomplex information. Thetetra-nucleotidetheory proposed byPhoebusLeveneAaron(1869 - 1940), stated that theDNA structureis regular andmonotonous,comprising a repeatingsequence offournitrogenous bases. Levenewas then one ofthe leading specialistsof nucleic acids;it was he whohad identifieddeoxyriboseas one componentof DNA.Proteins,which hadperceived theimmense diversity, seemed much bettercandidateto carrygenetic information (Fitzgerald-Hayes & Reichsman, 2009).

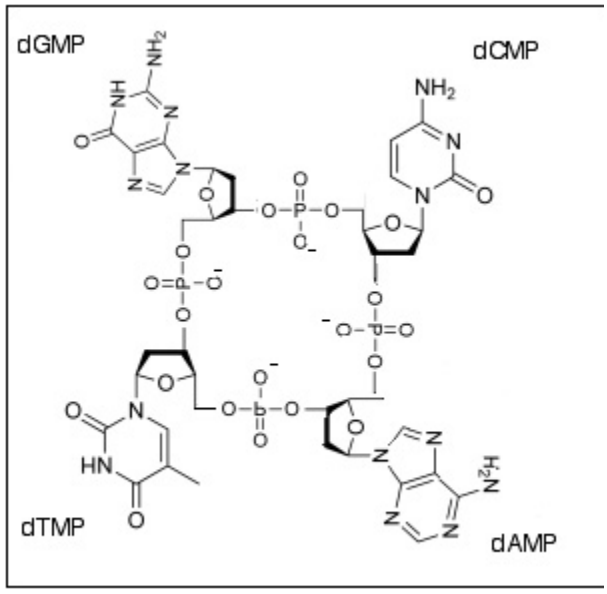
Levene Incorrect model Structure of DNA

Phoebus Levene (Russian biochemist) identified the chemical composition of the nuclei. He first discovered the sequencing of the major components of single nucleotide base of the phosphate and sugar. Also he had identified that the structure of the carbohydrate component of DNA (deoxyribose) and RNA (ribose) molecules are linked together. Structure of the molecular groups had been made in order to bind the component s of the nucleotide. These structures indicated that the components could be combined in the several alternate ways.

This structure model was introduced by the name of the Levine’s "polynucleotide" model. His tremendous work based on the using hydrolysis to investigate about the yeast nucleic acids. Levene had proposed that series of nucleotides were been composed by the nucleic acids. Each nucleotide was turned into the composition of the four phosphate groups, nitrogen bases, and a sugar molecule in the structure of the DNA.

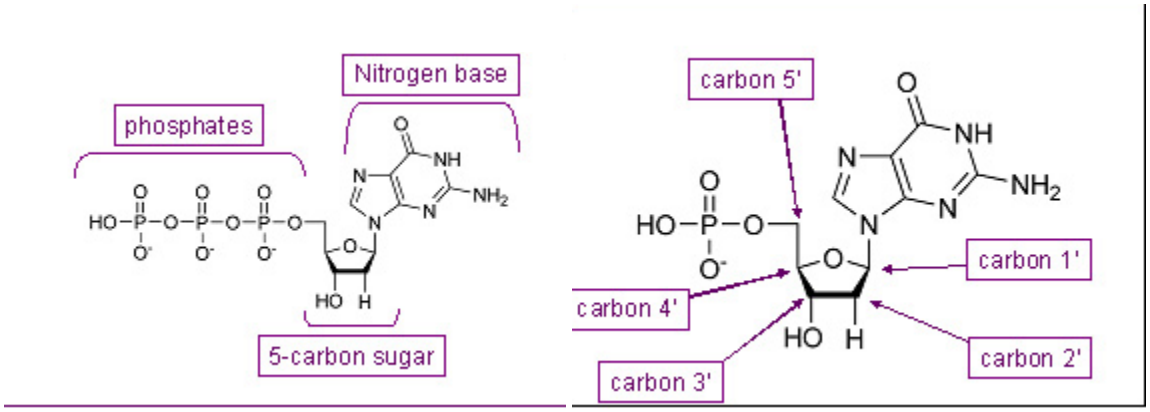
Initially his first proposal was introduced in 1919 which was related to the structure of nucleic acids. Indeed, Levene proposed that structure of the tetra-nucleotide were always linked in the sequence that is G-C-T-A-G-C-T-A. Simply, it happens because of the stretch of the DNA is highly variable. In spite of this realization of the research, proposal of Levene had deduced the polynucleotide structure. Levene had probed into further purification of the chemical composition of nucleic acid.

In his analysis he had found that chemical properties of the nuclei acid consists of nitrogen, phosphate group (PO4) and five – carbon sugar bases called DNA or the structure of the DNA. Levene had corrected to identify the three essential parts of a nucleotide made together in form of DNA. However, he proposed the four nucleotides (tetra-nucleotides) were made together in the form of the small circular molecules that was the foundation of the DNA.

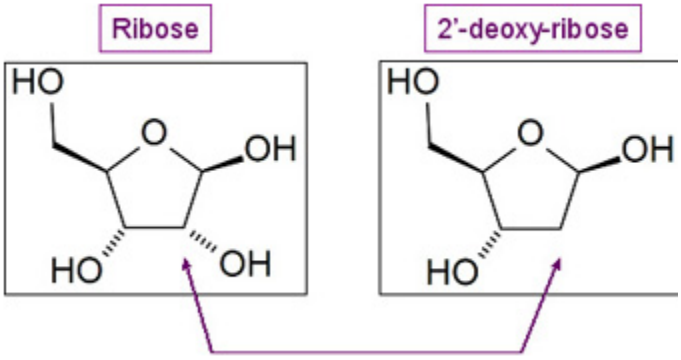


(Nathan Lents, 2009).

Phoebus Levene had incorrectly hypothesized that DNA was made of the circular tetra-nucleotides(Lents, 2009*).*



(Lents, 2009*).*

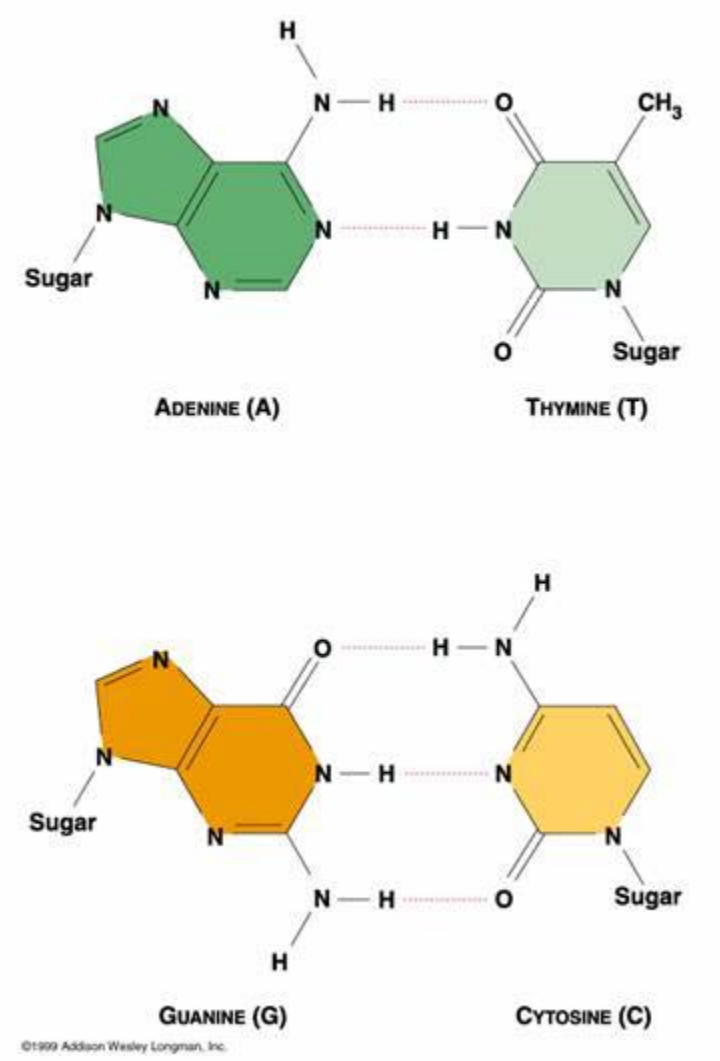


*(*Lents, 2009*).*

Chargaff Incorrect Model Structure of DNA

ChargaffwasanAustrian-bornbiochemistwho immigratedto the USA in1934. He was one of the Scientistsimmediatelygrasp theenormousscope ofAvery's work on the bacterialtransformation. WhenChargaff learned ofAvery'swork, Chargaffimmediatelyunderstood thatDNAplays a central rolein hereditarymechanisms, andhe decided tonow focus on the activities of hislaboratoryfor the study ofnucleic acids.

In 1950 hepublished his work onthe contentof nitrogenousbases of DNAin various species, achieved throughadvances inchromatography. He then showsthat the ratio A+T /G+Cisvariabledepending on the species, butconstantfor all membersof a given species. DNAisthe bearer of certain specificities; this moleculeis nota monotonouspolymer structure, so it is likely to containinformation (Chargaff, 1950). This work contributes tospread the idea thatthe DNA canbea carrierof genetic informationmolecule.



Chargaffalso shows thatthe C /GorA /Tisunlikealmostconstantandequal to onein all speciesstudied.Thisfinal point iscrucial for thedevelopment of the modelof the structureof DNA

byWatsonandCricka few years later. Followingthe success ofthis model,Chargaffis very reluctant torecognizethe wholepaternityfor which ithas never hadgreat esteem(followinghis first meetingwithWatsonandCrick, he wascompared with twoclowns). He continuedto claim fortheir own themodelbase pairing, so that there wasnever eventhought ofhim, and having demonstratedthatequaladenineandthyminereports,andcytosineguanine.

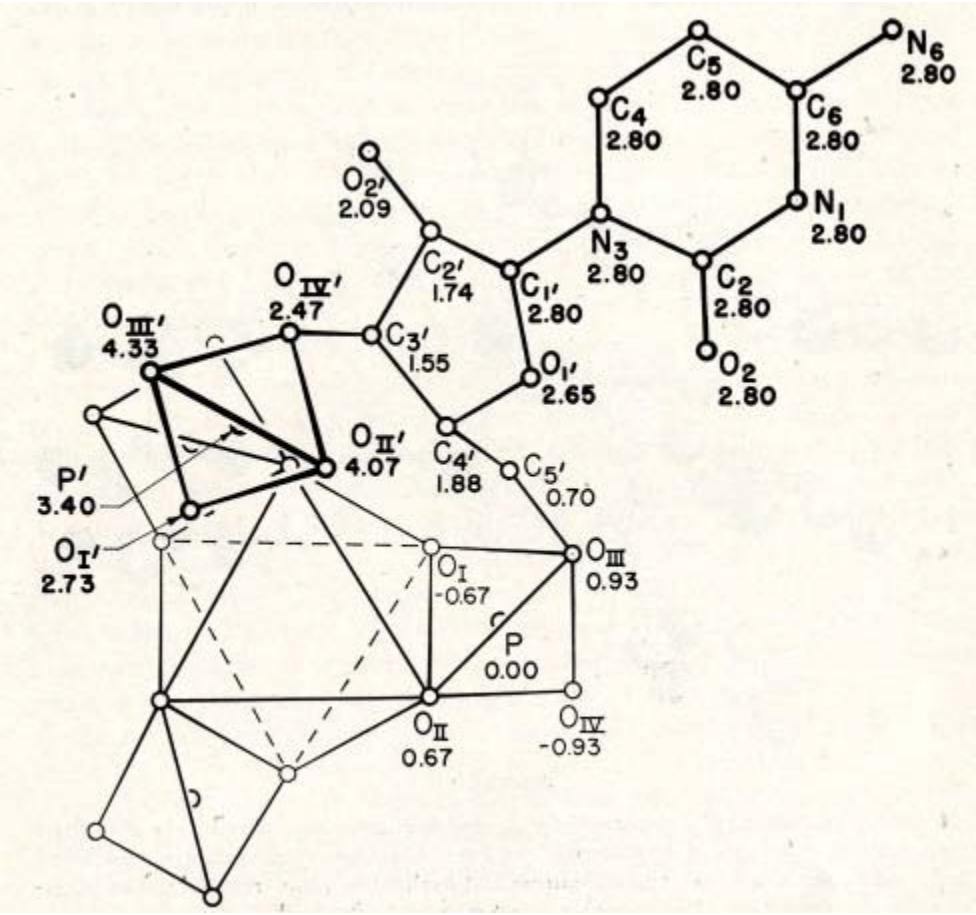
Pauling's Model Structure of DNA

Linus Pauling (1901 - 1994) was probably the greatest chemist of the century, who successfully landed various fields such as quantum physics, crystal structure and molecular biology. His first major contribution was regarding the chemical bond and he is particularly the first to recognize the importance of weak bonds. In 1940, Delbruck has developed the idea that stereospecific complementarity is at the base of molecular interactions in biology. He published two books that have revolutionized chemistry: The nature of the chemical bond (1939), and General Chemistry (1947). More than anything else, it helps to make the structure of molecules essential theme of biochemistry. It clarifies the structure of hundreds of minerals and is the discoverer of certain protein structures, such as the alpha helix and beta sheet (Pauling, 1953). He is also the first to provide a molecular explanation for a genetic disease: sickle cell anemias, in which he proposed as the origin altered haemoglobin.

At Cal Tech laboratory, Linus Pauling published an incorrect composition of DNA related to the chains of the 3 DNA wound in a helix. He had envisioned that the structure of the DNA could be a triple helix sowed the three strands of nucleotides. These are wrapped around each other. Significantly, Pauling got a Nobel Prize in order to correctly deduce the "alpha-helix" structure contained proteins. He proposed the triple helix model of DNA in the late 1953 which

was incorrect. Practice of the Pauling was depended on the building of the models of molecular compositions. Indeed, realization of the Linus depends on the insufficient results because the research data represented the overload research determined that structure of the Pauling turned out to be incorrect. The reason was he partly focused on the proteins rather than Structures of the DNA.

In the late 1952, Pauling was decided to attend the meeting of the Royal Society where he addressed the questions related to his structures of protein. He found that, there is no doubt the structures is difficult to define in such a manner but it can be bridged between an outer oxygen atom of a phosphate group and an outer oxygen atom of a one phosphate in the layer (Watson, 2012).



(Pauling, 1953)

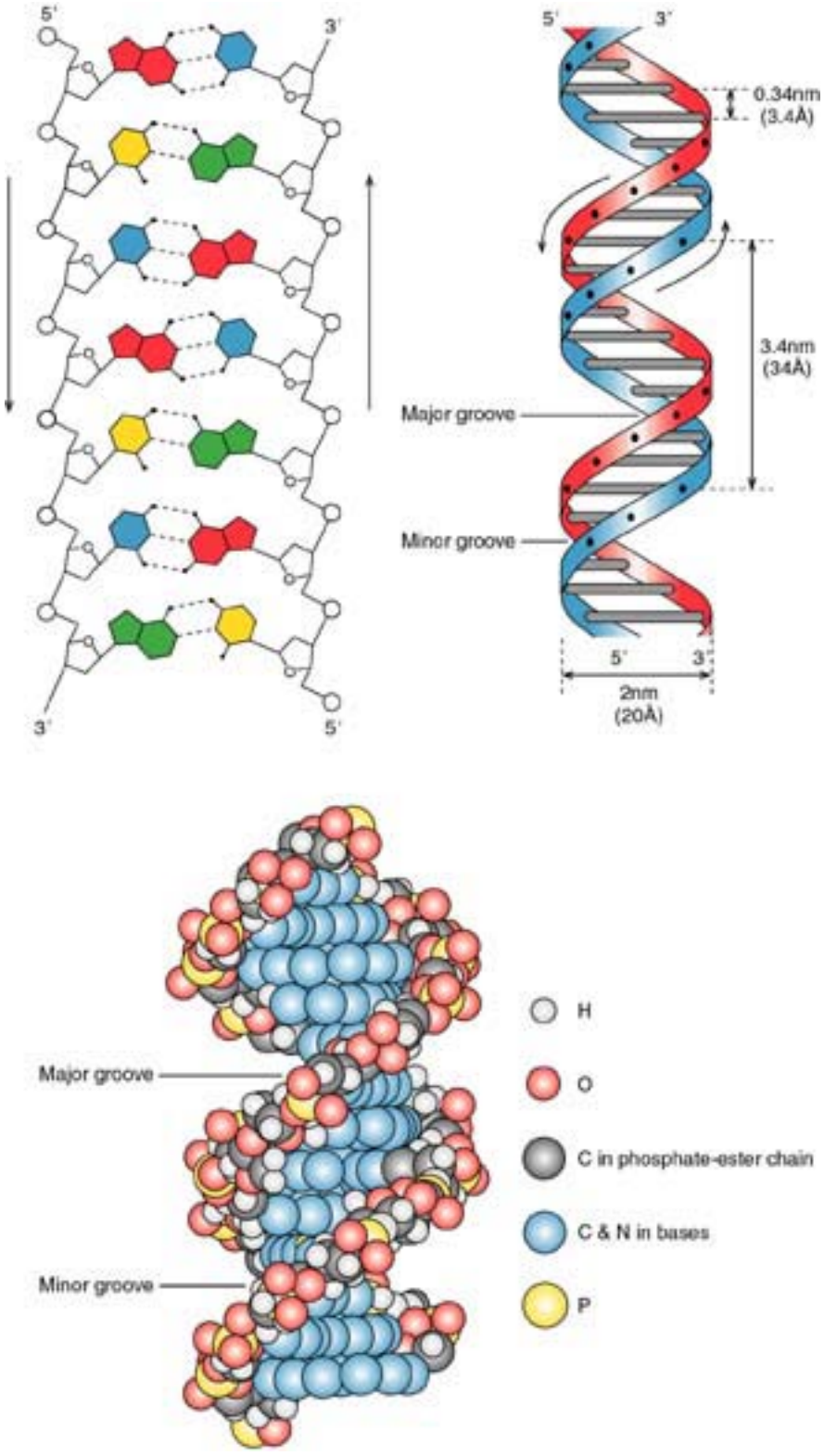
The atomic parameter showed in the above diagrams is one of the plans to represents the nuclei acid structure and has been showing one pyrimidine group , one ribofuranose group and four of the phosphate groups . However Pauling's research was the best solution of the research of the models of the DNA. Additionally, parameters of the phosphate groups are unsymmetrical so the distance between the oxygen and the phosphate is 1.45 Ångström in order to 2 inner oxygen atoms (Pauling, 1953).

In 1953, he published what he believed to be the structure: three channels ribose phosphate wrapping tightly around each other and the nitrogenous bases pointing radially

outwards from the beam. This totally misconception is partly explained by the fact that Pauling did not have access to the latest results of Rosalind Franklin.

Model developed by Watson andCrick

Thedouble helix structureof DNA iselucidated byWatsonandCrickin 1953,Watsondescribed in hisfascinating bookThe Double Helix(1968)the story of thegreatdiscovery madewithCrick. The two researchersthen havethe following:(i) the chemical composition of DNA (deoxyribose, nitrogen basesandphosphate groups); (ii) thediffraction patternsofX-ray crystallizedDNA blocks; (iii) the work ofErwinChargaff, whichhad shown thatany DNAmolecule, the number of adeninemoleculesequals the numberof moleculesofthymine, cytosineand thatisequal toguanine; (iv) inelectron microscopyanalysis, whichshowed thatthediameterofthe DNA moleculeis 20Å, suggesting that this moleculehad twochainsdeoxyribose phosphate.


5'
3'
3'
5'
5'
3'
0.34nm
(3.4Å)
3.4nm
(34Å)
Major groove
Minor groove
5'
3'
2nm
(20Å)
Major groove
Minor groove
H
O
C in phosphate-ester chain
C & N in bases
P

It issuccessivelydevelopingseveral molecularmodelsthatWatsonand Cricksuccessfullyprovide a structure thatsatisfies allcrystallographicand biochemical datathen available.This structureis nowknown to all,it has becomethe emblemof molecular biology: the two strandsconsistingofphosphate groupsand sugarsform a doublehelixwherethe orientations ofeach of the strandsare opposite.Oneach of the twosugarslinkedstrands arenitrogenous bases, eachstrand beingabasemaintainedvis-à-vis a base of the otherstrandby hydrogen bonding. Cytosinestill facesa guanine, adenineandthymineto. Both strandsof a DNAmoleculecomplementaryexpressed (Watson, 2012).

The order ofnucleotide basesdeterminesthe sequence ofamino acids inproteins. Aone-dimensionalstructurethus determinesthreedimensionalstructures. This paradoxical"information gain" is formedspontaneouslybytheprotein foldingastheir synthesis, according tothermodynamicconstraintsbytheirsequenceandthe environment in whichthey are synthesized. Living beingsthereforehaveadimensioninan informationsystem, entirely withinalinearsequence, that caneasilybecopiedorduplicated.Thislinear sequencefollowsthat of proteinsthatspontaneously adoptthethree-dimensional structurenecessary for theirfunction.

References

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